FIGURE 1.

Ammonifex degensii KC4 Phosphatase(3A1A=3A2A) Complete gene sequence

	ATGAGGGGAGCGGAGTGCGGATACTTCTCACCAACGATGACGGCATCTTTGCCGAGGGT
1	MetArgGlySerGlyValArgIleLeuLeuThrAsnAspAspGlyIlePheAlaGluGly
	CTGGGGGCTCTGCGCAAGATGCTGGAGCCCGTGGCTACCCTTTACGTGGTGGCTCCGGAC
21	LeuGlyAlaLeuArgLysMetLeuGluProValAlaThrLeuTyrValValAlaProAsp
	CGAGAGCGTAGCGGGCCAGCCATGCTATCACCGTTCACCGCCCCCTGCGGGTGCGGGAC
41	ArgGluArgSerAlaAlaSerHisAlaIleThrValHisArgProLeuArgValArgGlu
	GCGGGTTTTCGCAGCCCAGGCTTAAAGGCTGGGTAGTGGACGGTACCCCGGCCGACTGC
61	AlaGlyPheArgSerProArgLeuLysGlyTrpValValAspGlyThrProAlaAspCys
	GTCAAGCTGGGCCTGGAGGTACTTTTGCCCGAACGTCCAGATTTCCTGGTTTCGGGCATA
81	ValLysLeuGlyLeuGluValLeuLeuProGluArgProAspPheLeuValSerGlyIle
	AACTACGGGCCCAACCTGGGTACCGACGTACTTTACTCCGGCACCGTCTCGGCGGCCATA
101	AsnTyrGlyProAsnLeuGlyThrAspValLeuTyrSerGlyThrValSerAlaAlaIle
	GAAGGGTAATTAACGGCATTCCCTCGGTGGCCGTATCTTTGGCCACGCGGCGGGAGCCC
121	GluGlyValIleAsnGlyIleProSerValAlaValSerLeuAlaThrArgArgGluPro
	GACTATACCTGGGCGGCCCGGTTCGTCCTGGTCCTGGAGGAACTGCGAAAACACCAA
141	AspTyrThrTrpAlaAlaArgPheValLeuValLeuLeuGluGluLeuArgLysHisGl
	CTGCCCCAGGAACCCTGCTCAACGTCAACGTGCCCGACGGGGTGCCCCGGGGGTCAAC
161	LeuProProGlyThrLeuLeuAsnValAsnValProAspGlyValProArgGlyValLys
	GTGACCAAACTGGGAAGCGTACGCTACGTCAACGTGGTAGACTGCCGCACCGACCCTCGC
181	ValThrLysLeuGlySerValArgTyrValAsnValValAspCysArgThrAspProArg
	GGGAAGGCTTACTACTGGATGGCGGGAGAACCATTGGAGCTGGACGGCAACGACTCCGAA
201	GGGAAGGCTTACTACTACTACTACTACTACTACTACTACTACTACTA
	ACCGACGTCTGGGCGGTGCGAGAAGGCTATATTTCCGTAACACCGGTCCAGATCGACCT
221	ThrAspValTrpAlaValArgGluGlyTyrIleSerValThrProValGlnIleAspLet
	ACTAACTACGGCTTCCTGGAAGAACTCAAAAAATGGCGTTTCAAGGATATCTTTTCTTCT
241	ThrAsnTyrGlyPheLeuGluGluLeuLysLysTrpArgPheLysAspIlePheSerSer
	TAA

ȚAA 261 End 261

FIGURE 2

Methanococcus igneus Kol5 Phosphatase (9AlA) Complete Gene Sequence

	ATGTTGGATATACTGCTTGTTAATGATGATGGCATTTATTCAAATGGATTAATAGCTTTG
1	MetLeuAspIleLeuLeuValAsnAspAspGlyIleTyrSerAsnGlyLeuIleAlaLeu
	AAGGATGCATTATTGGAAAAATTTAATGCGAGGATTACTATTGTAGCCCCAACAAATCAG
21	LysAspAlaLeuLeuGluLysPheAsnAlaArgIleThrIleValAlaProThrAsnGln
	CAGAGTGGTATTGGTAGGGCAATAAGTTTATTCGAGCCGTTAAGGATAACTAAAACCAAA
41	GlnSerGlyIleGlyArgAlaIleSerLeuPheGluProLeuArgIleThrLysThrLys
	TTAGCAGATGGTTCTTGGGGATATGCAGTTTCAGGAACCCCAACAGATTGCGTTATATTG
61	LeuAlaAspGlySerTrpGlyTyrAlaValSerGlyThrProThrAspCysValIleLeu
	GGCATTTATGAGATATTAAAGAAGGTACCTGATGTAGTTATATCAGGAATAAACATTGGA
81	GlyIleTyrGluIleLeuLysLysValProAspValValIleSerGlyIleAsnIleGly
	GAAAACCTTGGGACTGAAATAACAACTTCTGGAACGTTGGGGGCTGCGTTTGAAGGGGCC
101	GluAsnLeuGlyThrGluIleThrThrSerGlyThrLeuGlyAlaAlaPheGluGlyAla
	CATCATGGGGCTAAGGCATTAGCATCACTCCAAGTTACCTCTGACCATCTAAAGTTT
121	HisHisGlyAlaLysAlaLeuAlaSerSerLeuGlnValThrSerAspHisLeuLysPhe
	AAAGAGGGGGAGACCCCAATAGACTTCACAGTCCCAGCAAGAATTACTGCAAATGTTGTT
141	LysGluGlyGluThrProIleAspPheThrValProAlaArgIleThrAlaAsnValVal
	GAGAAGATGTTGGATTATGATTTCCCATGTGATGTCGTCAACTTAAACATTCCAGAAGGA
161	GluLysMetLeuAspTyrAspPheProCysAspValValAsnLeuAsnIleProGluGly
	GCAACAGAAAAGACACCGATTGAAATCACAAGGTTGGCAAGGAAAATGTATACAACACAC
181	AlaThrGluLysThrProlleGluIleThrArgLeuAlaArgLysMetTyrThrThrHis
	GTTGAGGAAAGAATAGATCCAAGAGGGAGGAGTTATTATTGGATTGATGGGTATCCTATT
201	ValGluGluArgIleAspProArgGlyArgSerTyrTyrTrpIleAspGlyTyrProIle
	TTAGAGGAAGAGAGACACTGATGTCTATGTTAGAAGAAAAGGGACATATTTCTCTA
221	LeuGluGluGluAspThrAspValTyrValValArgArgLysGlyHisIleSerLeu
	ACCCCATTAACATTAGACACAACAATTAAAAATTTAGAGGAATTTAAGAAAAAATATGAG
241	ThrProLeuThrLeuAspThrThrIleLysAsnLeuGluGluPheLysLysLysTyrGlu
	AGAATATTAAATGAATGA
261	ArgIleLeuAsnGluEnd 266

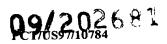


FIGURE 3

Thermococcus alcaliphilus AEDII12RA Phosphatase (18A)
Complete Gene Sequence

C	etMetMetGluPheThrArgGluGlyIleLysAlaAlaValGluAlaLeuGlnGlyLeu GAGAGATCTACGTAGTTGCCCCAATGTTTCAAAGGAGCGCAAGTGGAAGGGCAATGACC LyGluIleTyrValValAlaProMetPheGlnArgSerAlaSerGlyArgAlaMetThr TCCACAGACCTCTAAGGGCTAAAAGAATAAGTATGAACGGTGCAAAAGCAGCCTATGCT
G 21 G	lyGluIleTyrValValAlaProMetPheGlnArgSerAlaSerGlyArgAlaMetThr
21 G	
	THE REPORT OF THE PROPERTY OF
A'	CCACAGACCTCTAAGGGCTAAAAGAATAAGTATGAACGGTGCIZZZZGGTGC
41 I	leHisArgProLeuArgAlaLysArgIleSerMetAsnGlyAlaLysAlaAlaTyrAla
T'	PGGATGGAATGCCCGTTGATTGCGTTATCTTTGCCATGGCCAGATTTGGAGATTTCGAC
61 L	euAspGlyMetProValAspCysValIlePheAlaMetAlaArgPheGlyAspPheAsp
C'	MTGCAATAAGTGGTGTAAACTTGGGAGAAAACATGAGCACCGAGATAACGGTTTCCGGG
81 L	euAlaIleSerGlyValAsnLeuGlyGluAsnMetSerThrGluIleThrValSerGly
A	TGCAAGCGCTGCAATAGAGGCTGCAACCCAAGAGATCCCAAGCATTCCCATAAGCCTG
101 T	nrAlaSerAlaAlaIleGluAlaAlaThrGlnGluIleProSerIleProIleSerLeu
G	AGTTAATAGAGAAAAACACAAATTTGGTGAGGGCGAAGAGATTGACTTCTCAGCTGCC
121 G	uValAsnArgGluLysHisLysPheGlyGluGlyGluGluIleAspPheSerAlaAla
A	AGTATTTCCTAAGAAAAATCGCAACGGCGGTTTTAAAGAGAGGCCTCCCCAAAGGAGTC
141- L	GTATTTCCTAAGAAAAATCOGTATTATATTTTTTTTTTTT
G	ATATGCTGAACGTCAACGTCCCTTATGATGCAAATGAAAGGACAGAGATAGCTTTTACT
161 A	SPMetLeuAsnValAsnValProTyrAspAlaAsnGluArgThrGluIleAlaPheThr
C	SCCTGGCAAGAAGGATGTATAGGCCTTCTATTGAAGAGCGCATAGACCCAAAGGGGAAT
181 A	GLEUALAAGAAGGATGTATAGGETTEGLUGLUARGILeAspProLysGlyAsr
C	CTACTACTGGATAGTTGGAACTCAGTGCCCTAAGGAGGCATTAGAGCCGGGAACGGA
201 P	OTYTTYTTTPIleValGlyThrGlnCysProLysGluAlaLeuGluProGlyThrAsp
י מ	GTATGTAGTTAAAGTTGAGAGAAAAGTTAGCGTGACTCCAATAAACATTGATATGACA
221 Me	etTyrValValLysValGluArgLysValSerValThrProIleAsnIleAspMetThr
G	AAGAGTGAATTTAGACGAGATTAAAAGACTTTTAGAACTGTAG
241 A	aArgValAsnLeuAspGluIleLysArgLeuLeuGluLeuEnd 255

FIGURE 4

Thermococcus celer Phosphatase (25A1A) Complete Gene Sequence

	ATGAGAACCCTGACAATAAACACTGACGCGGAGGGGTTCGTTTTGAGGATTCTCCTGACG	
1	MetArgThrLeuThrIleAsnThrAspAlaGluGlyPheValLeuArgIleLeuLeuThr	20
	AACGACGATGGAATCTACTCCAACGGACTGCGCGCCGCTGTGAAAGCCCTGAGTGAG	
21	AsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaValLysAlaLeuSerGluLeu	40
	GGCGAAGTTTACGTCGTTGCCCCCCTCTTCCAGAGGAGCGCGAGCGGCAGGGCCATGACG	
41	GlyGluValTyrValValAlaProLeuPheGlnArgSerAlaSerGlyArgAlaMetThr	60
	CTCCACAGGCCGATAAGGGCCCAAGCGCGTTGACGTTCCCGGCGCAAAGATAGCCTACGGA	
61	LeuHisArgProIleArgAlaLysArgValAspValProGlyAlaLysIleAlaTyrGly	80
	ATAGATGGAACTCCTACTGACTGCGTGATTTTCGCCATAGCCCGCTTCGGGAGCTTTGGT	
81	IleAspGlyThrProThrAspCysValllePheAlalleAlaArgPheGlySerPheGly	100
	TTAGCCGTGAGCGGGATTAACCTCGGCGAGAACCTGAGCACCGAGATAACAGTCTCAGGG	
101	LeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThrGluIleThrValSerGly	120
	ACGGCCTCCGCTGCCATAGAGGCCTCAACTCATGGAATTCCGAGCATAGCGATTAGCCTT	
121	ThrAlaSerAlaAlaIleGluAlaSerThrHisGlyIleProSerIleAlaIleSerLeu	140
	GAGGTGGAGTGGAAGAAGACCCTCGGCGAGGGTGAGGGGGGTTGACTTCTCGGTCTCGACT	
141	GluValGluTrpLysLysThrLeuGlyGluGlyGluGlyValAspPheSerValSerThr	160
	CACTTCCTCAAGAGAATCGCGGGAGCCCTCTTGGAGAGAGGTCTTCCTGAGGGCGTTGAC	
161	HisPheLeuLysArgIleAlaGlyAlaLeuLeuGluArgGlyLeuProGluGlyValAsp	180
	ATGCTCAACGTCAACGTTCCGAGCGACGCGACGGAGAAACGGAGATAGCAATCACCCGC	
181	MetLeuAsnValAsnValProSerAspAlaThrGluGluThrGluIleAlaIleThrArg	200
	TTAGCCCGGAAGCGCTACTCCCCAACGGTCGAGGAGAGGATTGACCCCAAGGGCAACCCC	
201	LeuAlaArgLysArgTyrSerProThrValGluGluArgIleAspProLysGlyAsnPro	220
	TACTACTGGATTGTCGGCAAACTTGTCCAAGACTTCGAGCCAGGGACAGATGCCTACGCC	
221	TyrTyrTrpIleValGlyLysLeuValGlnAspPheGluProGlyThrAspAlaTyrAla	240
	CTGAAGGTCGAGAGGAAGGTCAGCGTCACGCCGATAAACATAGATATGACTGCGAGGGTG	
241	LeuLysValGluArgLysValSerValThrProIleAsnIleAspMetThrAlaArgVal	260
	GACTTTGAGGAGCTTGTAAGGGTTCTGTGGGTGTAA	
261	AspPheGluGluLeuValArgValLeuTrpValEnd 272	

FIGURE 5A

Thermococcus GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 1 of 2)

	ATGAAAGGAAAGTCTCTTGTTAGCGGTCTGTTGTTGGGTCTTTTAATTTTGAGCCTGATT	
1	MetLysGlyLysSerLeuValSerGlyLeuLeuGlyLeuLeuIleLeuSerLeuIle	20
	TCATTCCAGCCAAGCTTTGCATACTCCCCACACGGCGGTGTCAAAAACATCATAATCCTG	
21	SerPheGlnProSerPheAlaTyrSerProHisGlyGlyValLysAsnIleIleIleLeu	40
	GTTGGAGACGGCATGGGTCTTGGGCATGTAGAAATTACAAAGCTCGTTTATGGACACTTA	
41	ValGlyAspGlyMetGlyLeuGlyHisValGluIleThrLysLeuValTyrGlyHisLeu	60
	AACATGGAAAACTTTCCAGTTACTGGATTTGAGCTTACTGATTCCCTAAGTGGTGAAGTT	
61	AsnMetGluAsnPheProValThrGlyPheGluLeuThrAspSerLeuSerGlyGluVal	80
	ACAGATTCTGCTGCGGCAGGAACTGCAATATCCACTGGAGCTAAAACGTATAATGGTATG	100
81	ThrAspSerAlaAlaAlaGlyThrAlaIleSerThrGlyAlaLysThrTyrAsnGlyMet	100
	ATTTCAGTAACCAACATAACCGGAAAGATAGTTAACTTAACAACCCTACTTGAAGTGGCT	
101	IleSerValThrAsnIleThrGlyLysIleValAsnLeuThrThrLeuLeuGluValAla	120
	CAAGAGCTTGGGAAGTCAACAGGGCTGGTCACCACAACAAGGATTACCCATGCAACTCCA	
121	GlnGluLeuGlyLysSerThrGlyLeuValThrThrThrArgIleThrHisAlaThrPro	140
	GCAGTTTTTGCGTCCCATGTCCCAGATAGGGATATGGAGGGGGAGATACCCAAGCAACTC	
141	AlaValPheAlaSerHisValProAspArgAspMetGluGlyGluIleProLysGlnLeu	160
	ATAATGCACAAAGTTAACGTCTTGTTGGGTGGTGGAAGGGAGAAATTCGATGAGAAAAAT	
161	IleMetHisLysValAsnValLeuLeuGlyGlyGlyArgGluLysPheAspGluLysAsn	180
	TTGGAGCTGGCCAAAAAGCAGGGATACAAAGTAGTTTTCACGAAGGAAG	200
181	LeuGluLeuAlaLysLysGlnGlyTyrLysValValPheThrLysGluGluLeuGluLys	200
	GTTGAAGGAGATTATGTCCTAGGACTCTTTGCAGAAAGTCACATCCCTTACGTATTGGAT	226
201	ValGluGlyAspTyrValLeuGlyLeuPheAlaGluSerHisIleProTyrValLeuAsp	220
	AGAAAACCCGATGATGTTGGACTTTTAGAAATGGCCAAAAAGGCAATTTCAATACTCGAG	240
221	ArgLysProAspAspValGlyLeuLeuGluMetAlaLysLysAlaIleSerIleLeuGlu	240
	AAGAACCCGAGCGGATTCTTTCTCATGGTTGAGGGCGGAAGGATTGACCATGCAGCCCAT	
241	LysAsnProSerGlyPhePheLeuMetValGluGlyGlyArgIleAspHisAlaAlaHis	260
	GGAAACGATGTCGCATCGGTTGTTGCAGAAACTAAGGAGTTTGACGATGTTGTCAGATAC	200
261	GlyAsnAspValAlaSerValValAlaGluThrLysGluPheAspAspValValArgTyr	280
	GTGCTGGAATATCCGAAGAAGAGGGGAGATACCTTGGTAATAGTGCTTGCCGATCACGAA	200
281	ValLeuGluTyrProLysLysArgGlyAspThrLeuValIleValLeuAlaAspHisGlu	300
	ACTGGAGGTCTTGCAATAGGTCTAACGTATGGAAATGCAATCGATGAAGATGCCATAAGA	300
301	ThrGlyGlyLeuAlalleGlyLeuThrTyrGlyAsnAlalleAspGluAspAlalleArg	320
	AAAATAAAAGCAAGCACCTTTGAGGATGCCCAAAGAGGTTAAGGCAGGGAGTAGTGTAAAA	241
321	LysIleLysAlaSerThilieuArgMetProLysGluValLysAlaGlySerSerValLys	340

FIGURE 5B

Thermococcus GU5L5 Phosphatase (26A1A) Complete Gene Sequence (Part 2 of 2)

	GAGTCCTCAAAGGTATGCCGGATTTGTCCCAACAGAGGAAGAAGTCAGTATATTGAGAAT	
341	GluSerSerLysValCysArgIleCysProAsnArgGlyArgSerGlnTyrIleGluAsn	360
	GCGCTGCACTCGACAAACAAGTATGCCCTCTCAAATGCAGTAGCCGATGTTATAAACAGG	
361	AlaLeuHisSerThrAsnLysTyrAlaLeuSerAsnAlaValAlaAspValIleAsnArg	380
	CGTATTGGTGTTGGATTCACCTCCTATGAGCATACAGGAGTTCCAGTTCCGCTCTTAGCT	
381	ArglleGlyValGlyPheThrSerTyrGluHisThrGlyValProValProLeuLeuAla	400
	TACGGTCCCGGGGCAGAGAACTTCAGAGGTTTCTTACACCATGTGGATACAGCAAGATTA	
401	TyrGlyProGlyAlaGluAsnPheArgGlyPheLeuHisHisValAspThrAlaArgLeu	420
	GTTGCAAAGTTAATGCTCTTTGGAAGGAGGAATATTCCAGTTACCATTTCAAGCGTGAGC	
421	ValAlaLysLeuMetLeuPheGlyArgArgAsnIleProValThrIleSerSerValSer	440
	AGTGTTAAGGGAGACATAACCGGTGATTACAGGGTTGATGAGAAGGATGCCTACGTTACG	
441	SerValLysGlyAspIleThrGlyAspTyrArgValAspGluLysAspAlaTyrValThr	460
	CTCATGATGTTTCTCGGAGAAAAAGTGGATAATGAAAATTGAAAAAGAGAGTCGATATAGAC	
461	LeuMetMetPheLeuGlyGluLysValAspAsnGluIleGluLysArgValAspIleAsp	480
	AACAACGGCATGGTTGACTTAAATGACGTCATGTTGATTCTCCAGGAAGCTTGA	
481	AsnAsnGlyMetValAspLeuAsnAspValMetLeuIleLeuGlnGluAlaEnd 498	

20

320

340

FIGURE 6A

OC9a Phosphatase (27A3A)
Complete Gene Sequence (Part 1 of 2)

ATGCCAAGAAATATCGCCGCTGTATGCGCCCTGGCCGCTTTGTTAGGGTCGGCCTGGCCG

1 MetProArgAsnIleAlaAlaValCysAlaLeuAlaAlaLeuLeuGlySerAlaTrpAla

GCCAAAGTTGCCGTCTACCCCTACGACGGAGCCGCTTTGCTGGCGGGGGAGCGCTTCGAT

21	AlaLysValAlaValTyrProTyrAspGlyAlaAlaLeuLeuAlaGlyGlnArgPneAsp	40
	TTGCGCATAGAAGCCTCCGAGCTGAAAGGCAATTTAAAGGCTTACCGCATCACCCTGGAC	
41	LeuArgIleGluAlaSerGluLeuLysGlyAsnLeuLysAlaTyrArgIleThrLeuAsp	60
	GGCCAGCCTCTGGCGGGCCTCGAGCAAACCGCGCAGGGGGGCGGGC	
61	GlyGlnProLeuAlaGlyLeuGluGlnThrAlaGlnGlyAlaGlyGlnAlaGluTrpThr	80
	CTGCGCGGTGCCTTCCTGCGCCCTGGAAGCCACACCCTCGAGGTCAGCCTCACCGACGAC	
81	LeuArgGlyAlaPheLeuArgProGlySerHisThrLeuGluValSerLeuThrAspAsp	100
	GCTGGGGAGAGCAGGAAGAGCGTACGTTGGGAGGCTCGGCAGAACCTTCGCTTGCCCCGA	
101	AlaGlyGluSerArgLysSerValArgTrpGluAlaArgGlnAsnLeuArgLeuProArg	120
	GCGGCCAAGAATGTGATTCTCTTCATTGGCGACGGGATGGGCTGGAACACCCTCAACGCC	
121	AlaAlaLysAsnVallleLeuPhelleGlyAspGlyMetGlyTrpAsnThrLeuAsnAla	140
	GCCCGCATCATCGCCAAAGGCTTTAACCCCGAAAACGGTATGCCCAACGGAAACCTCGAG	
141	AlaArgIleIleAlaLysGlyPheAsnProGluAsnGlyMetProAsnGlyAsnLeuGlu	160
	ATCGAGAGTGGTTACGGTGGGATGGCTACCGTCACTACCGGCAGCTTTGATAGCTTCATC	
161	IleGluSerGlyTyrGlyGlyMetAlaThrValThrThrGlySerPheAspSerPheIle	180
	GCCGACTCAGCTAACTCGGCTTCTTCCATCATGACCGGGCAGAAGGTGCAGGTGAATGCC	
181	AlaAspSerAlaAsnSerAlaSerSerIleMetThrGlyGlnLysValGlnValAsnAla	200
	CTCAACGTTTACCCATCAAACCTCAAAGATACCCTGGCCTACCCCCGGATCGAAACCCTA	
201	LeuAsnValTyrProSerAsnLeuLysAspThrLeuAlaTyrProArgIleGluThrLeu	220
	GCGGAGATGCTCAAGCGGGTACGCGGGGCCAGCATTGGGGTAGTGACCACCACCTTCGGC	
221	AlaGluMetLeuLysArgValArgGlyAlaSerIleGlyValValThrThrThrPheGly	240
	ACCGACGCTACCCCGGCTTCACTCAACGCCCATACCCGCCGCGCGGGGTGATTACCAGGCT	
241	ThrAspAlaThrProAlaSerLeuAsnAlaHisThrArgArgArgGlyAspTyrGlnAla	260
	ATCGCCGACATGTACTTTGGTAGAGGCGGGTTCGGTGTTCCCTTGGATGTGATGCTCTTC	200
261	IleAlaAspMetTyrPheGlyArgGlyGlyPheGlyValProLeuAspValMetLeuPhe	280
	GGTGGTTCACGCGACTTCATCCCCCAGAGCACCCCTGGCTCGCGGGGGCAAGGATAGCACG	200
201	GlockSerArgAspPheIleProGlnSerThrProGlySerArgArgLysAspSerThr	300

GACTGGATTGCCGAATCCCAGAAGCTGGGCTACACCTTTGTCAGCACCCGCAGCGAGCTG
301 AspTrplleAlaGluSerGlnLysLeuGlyTyrThrPheValSerThrArgSerGluLeu

CTGGCGGCCAAACCCACCGATAAGCTCTTTTGGGCTCTTCAACATTGACAACTTCCCCAGC
321 LeuAlaAlaLysProThrAspLysLeuPheGlyLeuPheAsnIleAspAsnPheProSer

FIGURE 6B

OC9a Phosphatase (27A3A)
Complete Gene Sequence (Part 2 of 2)

	TACCTAGACCGCGCAGTGTGGAAGCGGCCCGAGATGCTGGGAAGCTTTACCGATATGCCC	
341	TyrLeuAspArgAlaValTrpLysArgProGluMetLeuGlySerPheThrAspMetPro	360
	TACCTCTGGGAGATGACCCAGAAAGCCGTGGAGGCTCTCTCCAGAAACGACAAAGGCTTT	
361	TyrLeuTrpGluMetThrGlnLysAlaValGluAlaLeuSerArgAsnAspLysGlyPhe	380
	TTCTTGATGGTTGAGGGGGGAATGGTGGATAAGTACGAGCACCCCTTGGACTGGCCCCGC	
381	PheLeuMetValGluGlyGlyMetValAspLysTyrGluHisProLeuAspTrpProArg	400
	GCACTTTGGGATGTACTCGAGCTGGACCGCGCGGTGGCTTGGGCCAAGGGCTATGCGGCC	
401	AlaLeuTrpAspValLeuGluLeuAspArgAlaValAlaTrpAlaLysGlyTyrAlaAla	420
	TCCCACCCGATACCCTGGTGATTGTCACCGCCGACCACGCTCACTCGATCTCGGTGTTT	
421	SerHisProAspThrLeuValIleValThrAlaAspHisAlaHisSerIleSerValPhe	440
	GGCGGTTACGACTACTCCAAGCAGGGCCGGGAGGGGGTGGGGGTTTATGAGGCCGCCAAG	
441	GlyGlyTyrAspTyrSerLysGlnGlyArgGluGlyValGlyValTyrGluAlaAlaLys	460
	TTCCCCACCTACGGCGACAAAAAAGACGCCAACGGCTTTCCCTTGCCCGACACCACTCGG	
461	PheProThrTyrGlyAspLysLysAspAlaAsnGlyPheProLeuProAspThrThrArg	480
	GGAATCGCGGTAGGCTTCGGGGCCACGCCGGATTACTGTGAAACCTACCGGGGCCGCGAG	
481	GJyIleAlaValGlyPheGlyAlaThrProAspTyrCysGluThrTyrArgGlyArgGlu	500
	GTCTACAAAGACCCCACCATCTCCGACGCCAAAGGTGGTTACGTGGCCAACCCTGAGGTC	
501	ValTyrLysAspProThrIleSerAspGlyLysGlyGlyTyrValAlaAsnProGluVal	520
-	TGCAAGGAGCCGGGCCTTCCAACGTACCGCAACTCCCAGTAGATAGCGCCCAGGGGGTG	
521	CysLysGluProGlyLeuProThrTyrArgGlnLeuProValAspSerAlaGlnGlyVal	540
	CACACGGCTGATCCCATGCCGCTGTTTGCCTTTGGCGTGGGGTCTCAGTTCTTCAATGGC	
541	HisThralaAspProMetProLeuPheAlaPheGlyValGlySerGlnPhePheAsnGly	560
	CTCATCGACCAGACCGAGATCTTCTTCCGCATGGCCCAGGCCCTAGGGTTCAACCCCCAC	
561	LeuIleAspGlnThrGluIlePhePheArgMetAlaGlnAlaLeuGlyPheAsnProHis	580
	CTCGAGAAGCCTTAA	
581	LeuGluLysProEnd 585	

FIGURE 7

Mll TL Phosphatase (29A1A=29A2A) Complete Gene Sequence

	ATGTATAAATGGATTATTGAGGGTAAGCTTGCCCAAGCACCTTTTCCAAGCCTAGGTGAA	
1	MetTyrLysTrpIleIleGluGlyLysLeuAlaGlnAlaProPheProSerLeuGlyGlu	20
	CTAGCCGATCTCAAAAGACTTTTCGACGCCATTATTGTTCTTACAATGCCGCATGAACAA	
21	LeuAlaAspLeuLysArgLeuPheAspAlaIleIleValLeuThrMetProHisGluGln	40
	CCGCTTAATGAGAAATATATCGAGATATTAGAGAGCCATGGATTCCAAGTCCTCCATGTC	
41	ProLeuAsnGluLysTyrIleGluIleLeuGluSerHisGlyPheGlnValLeuHisVal	60
	CCCACGCTCGACTTTCATCCTTTAGAACTCTTCGACCTTTTGAAAACAAGCATATTCATT	80
61	ProThrLeuAspPheHisProLeuGluLeuPheAspLeuLeuLysThrSerIlePheIle	80
	GATGAAAACCTGGAGAGATCCCACAGAGTGCTTGTCCACTGCATGGGAGGCATAGGCCGG	100
81	AspGluAsnLeuGluArgSerHisArgValLeuValHisCysMetGlyGlyIleGlyArg	100
	AGCGGGCTTGTAACTGCTGCGTACTTAATATTCAAAGGTTATGATATTTACGACGCGGTA	120
101	SerGlyLeuValThrAlaAlaTyrLeuIlePheLysGlyTyrAspIleTyrAspAlaVal	
	AAGCATGTGAGAACGGTAGTGCCTGGTGCTATTGAAAACAGAGGGCAAGCGTTAATGCTT	140
121	LysHisValArgThrValValProGlyAlaIleGluAsnArgGlyGlnAlaLeuMetLeu	140
	GAGAACTACTATACCCTGGTCAAAAGTTTCAACAGAGAGTTGCTGAGAGACTACGGGAAG	160
141	GluAsnTyrTyrThrLeuValLysSerPheAsnArgGluLeuLeuArgAspTyrGlyLys	
	AAAATTTTCACGCTCGGTGACCCGAAGGCGGTTCTCCACGCTTCTAAGACGACTCAGTTC	180
161	LysIlePheThrLeuGlyAspProLysAlaValLeuHisAlaSerLysThrThrGlnPhe	
	ACGATTGAACTCTTAAGCAACTTACACGTCAACGAGGCGTTTTCAATCAGTGCGATGGCT	200
181	ThrIleGluLeuLeuSerAsnLeuHisValAsnGluAlaPheSerIleSerAlaMetAla	
	CAATCACTGCTCCACTTTCACGACGTAAAAGTCCGCTCTAAACTGAAAGAAGTATTCGAA	220
201	GlnSerLeuLeuHisPheHisAspValLysValArgSerLysLeuLysGluValPheGlu	
	AACATGGAATTCTCATCCGCCTCAGAGGAGGTTCTGTCATTTATTCACCTACTCGATTTC	240
221	AsnMetGluPheSerSerAlaSerGluGluValLeuSerPheIleHisLeuLeuAspPhe	2.0
	TATCAGGATGGCAGGGTTGTTTTAACCATTTACGATTATCTCCCCGATAGGGTGGATTTG	260
241	TyrGlnAspGlyArgValValLeuThrIleTyrAspTyrLeuProAspArgValAspLeu	
	ATTTTATTGTGTAAGTGGGGTTGTGATAAAATAGTTGAACTCTCGTCTTCAGCGAAGAAA	280
261	IleLeuLeuCysLysTrpGlyCysAspLysIleValGluValSerSerSerAlaLysLys	200
	ACCGTTGAGAAGCTTGTAGGAAGAAAGGTTTCCCTATCCTGGGCTAATTACTTAGACTAT	300
281	ThrValGluLysLeuValGlyArgLysValSerLeuSerTrpAlaAsnTyrLeuAspTyr	300
	GTTTAG	

301 ValEnd 302

FIGURE 8

Thermococcus CL-2 Phosphatase (30A1A) Complete Gene Sequence

	ATGAGAATCCTCCTCACCAACGACGACGGCATCTATTCCAACGGTCTGCGCGCGGCGGTG	
1	MetArgIleLeuLeuThrAsnAspAspGlyIleTyrSerAsnGlyLeuArgAlaAlaVal	20
	AAGGGCCTGAGCGAGCTCGGCGAGGTCTACGTCGTCGCCCCGCTCTTCCAGAGGAGCGCG	
21	LysGlyLeuSerGluLeuGlyGluValTyrValValAlaProLeuPheGlnArgSerAla	40
	AGCGGTCGGGCGATGACCCTACACAGGCCGATAAGGGCAAAGAGGGTTGACGTTCCCGGC	6.0
41	SerGlyArgAlaMetThrLeuHisArgProIleArgAlaLysArgValAspValProGly	60
	GCGAAGATAGCGTATGGCATAGACGGAACGCCGACCGACTGCGTGATTTTTGCCATCGCC	0.0
61	AlaLysIleAlaTyrGlyIleAspGlyThrProThrAspCysValIlePheAlaIleAla	80
	CGCTTCGGCGACTTTGATCTGGCGGTCAGCGGGATAAACCTAGGCGAGAACCTGAGCACG	
81	ArgPheGlyAspPheAspLeuAlaValSerGlyIleAsnLeuGlyGluAsnLeuSerThr	100
	GAGATAACCGTCTCCGGAACGGCCTCGGCGGCGATAGAGGCTTCCACCCAC	
101	GAGATAACCGTCTCCGGAACGGCCTCGGCCCGCGCGCGCG	120
	AGTGTAGCTATAAGCCTCGAGGTCGAGTGGAAGAAGACCCTCGGCGAGGGGGAGGGTATT	
121	AGTGTAGCTATAAGCCTCGAGGTCGAGTCGAGTCGAGGTCAGGTCAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG	140
	GACTTCTCGGTTTCAGCACACTTCCTGAGAAGGATAGCGACGGCTGTCCTTAAGAAGGGC	
141	AspPheSerValSerAlaHisPheLeuArgArgIleAlaThrAlaValLeuLysLysGly	160
	CTGCCTGAAGGGGTGGACATGCTCAACGTGAACGTCCCTAGCGACGCCAGCGAGGGGACT	
161	CTGCCTGAAGGGGTGGACATGCTCAAAGTTAAAGTAAAAAAAA	180
	GAGATCGCCATAACGCGCCTCGCGAGGAAGCGCTATTCTCCGACGATAGAGGAGAGATA	
181	GAGATCGCCATAACGCGCCTCGCGAAGAACGCTCGCAAGAACGCCCATAACGCGCCTCGCGAAGAACGCTCGCAAGAACGCCCTCGCGAAGAACGCCCATAACGCCGCCTCGCGAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACGCCCAAGAACAAC	200
	GACCCCAAGGGCAACCCCTACTACTGGATCGTTGGCAGGCTCGTCCAGGAGTTCGAGCCG	
201	AspProLysGlyAsnProTyrTyrTrpIleValGlyArgLeuValGlnGluPheGluPro	220
	GGCACGGACGCCTACGCTCTGAAAGTCGAGAGAAAGGTCAGCGTCACGCCCATAAACATC	_
221	GGCACGGACGCCTACGCTCTGAAAGTCSTONATGLYSValSerValThrProIleAsnIle GlyThrAspAlaTyrAlaLeuLysValGluArgLysValSerValThrProIleAsnIle	240
	CACATTCA CTCCCACCCTTGACTTTGAGAACCTTCAAAGGCTTCTGAGCCTGTGA	
241	AspMetThrAlaArgValAspPheGluAsnLeuGlnArgLeuLeuSerLeuEnd 258	
C 4 1	Dapisces in the mineral property of	

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FIGURE 9

Aquifex VF-5 Phosphatase (34A1A) Complete Gene Sequence

	ATGGAAAACTTAAAAAAGTACCT'AGAAGTTGCAAAAATAGCCGCGCTCGCGGGTGGGCAG	
1		20
	GTTCTGAAAGAAACTTCGGAAAGGTAAAAAAGGAAAAACATAGAGGAAAAAGGGGAAAAAG	
21	ValLeuLysGluAsnPheGlyLysValLysLysGluAsnIleGluGluLysGlyGluLys	40
	GACTTTGTAAGTTACGTGGATAAAACTTCAGAGGAAAGGATAAAGGAGGTGATACTCAAG	
41	AspPheValSerTyrValAspLysThrSerGluGluArgIleLysGluValIleLeuLys	60
	TTCTTTCCCGATCACGAGGTCGTAGGGGAAGAGATGGGTGCGGAGGGAAGCGAAGCGAA	
61	PhePheProAspHisGluValValGlyGluGluMetGlyAlaGluGlySerGlySerGlu	80
	TACAGGTGGTTCATAGACCCCCTTGACGGCACAAAGAACTACATAAACGGTTTTCCCATC	
81	TyrArgTrpPheIleAspPrpLeuAspGlyThrLysAsnTyrIleAsnGlyPheProIle	100
	TTTGCCGTATCAGTGGGACTTGTTAAGGGAGAAGAGCCAATTGTGGGTGCGGTTTACCTT	
101	PheAlaValSerValGlyLeuValLysGlyGluGluProIleValGlyAlaValTyrLeu	120
	CCTTACTTTGACAAGCTTTACTGGGGTGCTAAAGGTCTCGGGGGCTTACGTAAACGGAAAG	
121	ProTyrPheAspLysLeuTyrTrpGlyAlaLysGlyLeuGlyAlaTyrValAsnGlyLys	140
	AGGATAAAGGTAAAGGACAATGAGAGTTTAAAGCACGCCGGAGTGGTTTACGGATTTCCC	
141	ArgIleLysValLysAspAsnGluSerLeuLysHisAlaGlyValValTyrGlyPhePro	160
	TCTAGGAGCAGGAGGACATATCTATCTACTTGAACATATTCAAGGATGTCTTTTACGAA	
161	SerArgSerArgArgAspIleSerIleTyrLeuAsnIlePheLysAspValPheTyrGlu	180
	GTTGGCTCTATGAGGAGACCCGGGGCTGCTGCGGTTGACCTCTGCATGGTGGCGGAAGGG	
181	ValGlySerMetArgArgProGlyAlaAlaAlaValAspLeuCysMetValAlaGluGly	200
	ATATTTGACGGGATGATGGAGTTTGAAATGAAGCCGTGGGACATAACCGCAGGGCTTGTA	
201	IlePheAspGlyMetMetGluPheGluMetLysProTrpAspIleThrAlaGlyLeuVal	220
	ATACTGAAGGAAGCCGGGGGCGTTTACACACTTGTGGGAGAACCCTTCGGAGTTTCGGAC	
221	IleLeuLysGluAlaGlyGlyValTyrThrLeuValGlyGluProPheGlyValSerAsp	240
	ATAATTGCGGGCAACAAAGCCCTCCACGACTTTATACTTCAGGTAGCCAAAAAGTATATG	
241	IlelleAlaGlyAsnLysAlaLeuHisAspPheIleLeuGlnValAlaLysLysTyrMet	260
	GAAGTGGCGGTGTGA	
261	GluValAlaValEnd 265	